

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/569,791  
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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/569,791

DATE: 12/05/2006  
TIME: 12:30:38

Input Set : N:\efs\12\_05\_06\10569791\_efs\2006112012540305PUS1.txt  
Output Set: N:\CRF4\12052006\J569791.raw

3 <110> APPLICANT: Yorimasa SUWA et al.  
5 <120> TITLE OF INVENTION: TARGET PROTEIN OF ANTIDIABETIC AND NOVEL ANTIDIABETIC  
"INSUFUL"  
7 <130> FILE REFERENCE: 1254-0305PUS1  
9 <140> CURRENT APPLICATION NUMBER: 10/569,791  
10 <141> CURRENT FILING DATE: 2006-02-27  
12 <150> PRIOR APPLICATION NUMBER: PCT/JP04/16996  
13 <151> PRIOR FILING DATE: 2004-11-16  
15 <150> PRIOR APPLICATION NUMBER: JP 2003/402164  
16 <151> PRIOR FILING DATE: 2003-12-01  
18 <160> NUMBER OF SEQ ID NOS: 3  
20 <170> SOFTWARE: PatentIn Ver. 2.0  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 2617  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Homo sapiens  
27 <400> SEQUENCE: 1  
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30 gggttgattt ggcacaaacc gcccgaccca gggggccggtg cgcgtgtgga aggggaagca 180  
31 ctccccctgtt ggtcgccctgg aggtgcgctg gaggaggggg tgacataacc agggactcga 240  
32 ggtccgccgtt ggaatgatc cacgaactgc tcttggctct gagcgggtac cctgggtcca 300  
33 ttttcacctg gaacaagcgg agtggcctgc aggtatcgcga ggactccctt ttcctccacc 360  
34 ccagtgagac cagtgtcctg aatcgactct gccggctcgg cacagactat attcgcttca 420  
35 ctgagttcat tgaacagttac acggggccatg tgcaacagca ggatcaccat ccatctcaac 480  
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38 atctctccat atcacatgtc aactacttcc tagaccagtt ccagcttctt tttccctctg 660  
39 ttaggttgtt agtagaaacaa attaaaagtc aaaagattca tggttgtcaa atcctggaaa 720  
40 cagtctacaa acacagctgt ggggggttgc ctccctgttcg aagtgcactg gaaaaaatcc 780  
41 tggccgtttt tcatgggggtc atgtataaac agctctcagc ctggatgctc catggactcc 840  
42 tcttggacca gcatgaagaa ttctttatca aacagggggcc atcttctgtt aatgtcagtg 900  
43 cccagccaga agaggacgag gaggatctgg gcattggggg actgacagga aaacaactga 960  
44 gagaactgca ggacttgcgc ctgattgagg aagagaacat gctggcacca tctctgaagc 1020  
45 agttttccct acgagttggag atttgccat cctacattcc agtgagggtt gctgaaaaaa 1080  
46 tccttatttgt tggagaatct gtccagatgt ttgagaatca aatgtgaac ctgactagaa 1140  
47 aaggatccat tttgaaaaac caggaagaca cttttctgc agagctgcac cgtctcaagc 1200  
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51 ctcacacat gttgaaaaca ccacccactg cagtaactga gcatgatgtg aatgtggcct 1440  
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54 cttctcggtt aacttctccc cgggaagccc ctgcattgg ctggcagcc ctaggtctt 1620

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55 cctacaaaagt acagtggcca ctacatattc tcttacccccc agctgtccctg gaaaagtaca 1680  
 56 atgttggttt taagtactta ctgagtgtgc gccgggtgca agctgagctg cagcaactgct 1740  
 57 gggccctaca aatgcagcgc aagcacctca agtcaaacca gactgatgca atcaagtggc 1800  
 58 gcctaagaaa tcacatggca tttttggtgg ataatctca gtactatctc caggttagatg 1860  
 59 tggggagtc tcagttctcc cagctgcttc atcagatcaa ttctacccga gactttgaaa 1920  
 60 gcatccgatt ggctcatgac cacttcctga gcaatttgct ggctcaatcc tttatcctat 1980  
 61 tggaaacctgt gtttcaactgc ctgaatgaaa tccttagatct ctgtcacagt ttttggc 2040  
 62 tggtcagtca gaaccttaggc ccactggatg agcgtggagc cgccccagctg agcattctcg 2100  
 63 tgaaggggctt tagccgcccag tcttcactcc tggtaagat tctctccagg gttcggaaatc 2160  
 64 atcagatcaa ctcagatttgc gctcaactac tggttacgact agattataac aaataactata 2220  
 65 cccaggctgg tggaaactctg ggcagttcg ggatgtgaaa atttctggct cataaaattga 2280  
 66 aataacagcc acgttcccaa gggtgttaaca gaagattcaa aacatcccat tctagccaca 2340  
 67 cacaataaaa tatctgcggc tttagttaga gacttacact tttctcctag aagcagttac 2400  
 68 tgaacatcca ggagtacaac tccttcccat cattcccatg tggaaagggtc tctccatca 2460  
 69 aggagaacat gtggcatctc tgatccttta cattgagaac atttggta tatgttcatt 2520  
 70 tattcaatag tcatttatttgc acgacacactt acgtacccctt gttactgttca agctgtggga 2580  
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73 &lt;210&gt; SEQ ID NO: 2

74 &lt;211&gt; LENGTH: 667

75 &lt;212&gt; TYPE: PRT

76 &lt;213&gt; ORGANISM: Homo sapiens

78 &lt;400&gt; SEQUENCE: 2

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 83 20 25 30  
 85 Phe Leu His Pro Ser Glu Thr Ser Val Leu Asn Arg Leu Cys Arg Leu  
 86 35 40 45  
 88 Gly Thr Asp Tyr Ile Arg Phe Thr Glu Phe Ile Glu Gln Tyr Thr Gly  
 89 50 55 60  
 91 His Val Gln Gln Gln Asp His His Pro Ser Gln Gln Gly Gln Gly  
 92 65 70 75 80  
 94 Leu His Gly Ile Tyr Leu Arg Ala Phe Cys Thr Gly Leu Asp Ser Val  
 95 85 90 95  
 97 Leu Gln Pro Tyr Arg Gln Ala Leu Leu Asp Leu Glu Gln Glu Phe Leu  
 98 100 105 110  
 100 Gly Asp Pro His Leu Ser Ile Ser His Val Asn Tyr Phe Leu Asp Gln  
 101 115 120 125  
 103 Phe Gln Leu Leu Phe Pro Ser Val Met Val Val Val Glu Gln Ile Lys  
 104 130 135 140  
 106 Ser Gln Lys Ile His Gly Cys Gln Ile Leu Glu Thr Val Tyr Lys His  
 107 145 150 155 160  
 109 Ser Cys Gly Gly Leu Pro Pro Val Arg Ser Ala Leu Glu Lys Ile Leu  
 110 165 170 175  
 112 Ala Val Cys His Gly Val Met Tyr Lys Gln Leu Ser Ala Trp Met Leu  
 113 180 185 190  
 115 His Gly Leu Leu Leu Asp Gln His Glu Glu Phe Phe Ile Lys Gln Gly  
 116 195 200 205  
 118 Pro Ser Ser Gly Asn Val Ser Ala Gln Pro Glu Glu Asp Glu Asp

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121	Leu	Gly	Ile	Gly	Gly	Leu	Thr	Gly	Lys	Gln	Leu	Arg	Glu	Leu	Gln	Asp
122	225			230				235								240
124	Leu	Arg	Leu	Ile	Glu	Glu	Glu	Asn	Met	Leu	Ala	Pro	Ser	Leu	Lys	Gln
125				245					250							255
127	Phe	Ser	Leu	Arg	Val	Glu	Ile	Leu	Pro	Ser	Tyr	Ile	Pro	Val	Arg	Val
128				260				265								270
130	Ala	Glu	Lys	Ile	Leu	Phe	Val	Gly	Glu	Ser	Val	Gln	Met	Phe	Glu	Asn
131		275			280											285
133	Gln	Asn	Val	Asn	Leu	Thr	Arg	Lys	Gly	Ser	Ile	Leu	Lys	Asn	Gln	Glu
134		290			295											300
136	Asp	Thr	Phe	Ala	Ala	Glu	Leu	His	Arg	Leu	Lys	Gln	Gln	Pro	Leu	Phe
137		305				310				315						320
139	Ser	Leu	Val	Asp	Phe	Glu	Gln	Val	Val	Asp	Arg	Ile	Arg	Ser	Thr	Val
140				325				330								335
142	Ala	Glu	His	Leu	Trp	Lys	Leu	Met	Val	Glu	Glu	Ser	Asp	Leu	Leu	Gly
143				340				345								350
145	Gln	Leu	Lys	Ile	Ile	Lys	Asp	Phe	Tyr	Leu	Leu	Gly	Arg	Gly	Glu	Leu
146				355				360								365
148	Phe	Gln	Ala	Phe	Ile	Asp	Thr	Ala	Gln	His	Met	Leu	Lys	Thr	Pro	Pro
149		370			375				380							
151	Thr	Ala	Val	Thr	Glu	His	Asp	Val	Asn	Val	Ala	Phe	Gln	Gln	Ser	Ala
152		385			390				395							400
154	His	Lys	Val	Leu	Leu	Asp	Asp	Asp	Asn	Leu	Leu	Pro	Leu	Leu	His	Leu
155				405					410							415
157	Thr	Ile	Glu	Tyr	His	Gly	Lys	Glu	His	Lys	Ala	Asp	Ala	Thr	Gln	Ala
158				420				425								430
160	Arg	Glu	Gly	Pro	Ser	Arg	Glu	Thr	Ser	Pro	Arg	Glu	Ala	Pro	Ala	Ser
161				435				440								445
163	Gly	Trp	Ala	Ala	Leu	Gly	Leu	Ser	Tyr	Lys	Val	Gln	Trp	Pro	Leu	His
164				450				455								460
166	Ile	Leu	Phe	Thr	Pro	Ala	Val	Leu	Glu	Lys	Tyr	Asn	Val	Val	Phe	Lys
167		465				470				475						480
169	Tyr	Leu	Leu	Ser	Val	Arg	Arg	Val	Gln	Ala	Glu	Leu	Gln	His	Cys	Trp
170				485					490							495
172	Ala	Leu	Gln	Met	Gln	Arg	Lys	His	Leu	Lys	Ser	Asn	Gln	Thr	Asp	Ala
173				500				505								510
175	Ile	Lys	Trp	Arg	Leu	Arg	Asn	His	Met	Ala	Phe	Leu	Val	Asp	Asn	Leu
176				515				520								525
178	Gln	Tyr	Tyr	Leu	Gln	Val	Asp	Val	Leu	Glu	Ser	Gln	Phe	Ser	Gln	Leu
179				530				535								540
181	Leu	His	Gln	Ile	Asn	Ser	Thr	Arg	Asp	Phe	Glu	Ser	Ile	Arg	Leu	Ala
182		545				550				555						560
184	His	Asp	His	Phe	Leu	Ser	Asn	Leu	Leu	Ala	Gln	Ser	Phe	Ile	Leu	Leu
185				565				570								575
187	Lys	Pro	Val	Phe	His	Cys	Leu	Asn	Glu	Ile	Leu	Asp	Leu	Cys	His	Ser
188				580				585								590
190	Phe	Cys	Ser	Leu	Val	Ser	Gln	Asn	Leu	Gly	Pro	Leu	Asp	Glu	Arg	Gly
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193 Ala Ala Gln Leu Ser Ile Leu Val Lys Gly Phe Ser Arg Gln Ser Ser  
194 610 615 620  
196 Leu Leu Phe Lys Ile Leu Ser Ser Val Arg Asn His Gln Ile Asn Ser  
197 625 630 635 640  
199 Asp Leu Ala Gln Leu Leu Leu Arg Leu Asp Tyr Asn Lys Tyr Tyr Thr  
200 645 650 655  
202 Gln Ala Gly Gly Thr Leu Gly Ser Phe Gly Met  
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206 <210> SEQ ID NO: 3  
207 <211> LENGTH: 667  
208 <212> TYPE: PRT  
209 <213> ORGANISM: Homo sapiens  
211 <400> SEQUENCE: 3  
213 Met Ile His Glu Leu Leu Ala Leu Ser Gly Tyr Pro Gly Ser Ile  
214 1 5 10 15  
217 Phe Thr Trp Asn Lys Arg Ser Gly Leu Gln Val Ser Gln Asp Phe Pro  
218 20 25 30  
221 Phe Leu His Pro Ser Glu Thr Ser Val Leu Asn Arg Leu Cys Arg Leu  
222 35 40 45  
225 Gly Thr Asp Tyr Ile Arg Phe Thr Glu Phe Ile Glu Gln Tyr Thr Gly  
226 50 55 60  
229 His Val Gln Gln Gln Asp His His Pro Ser Gln Gln Gly Gln Gly  
230 65 70 75 80  
233 Leu His Gly Ile Tyr Leu Arg Ala Phe Cys Thr Gly Leu Asp Ser Val  
234 85 90 95  
237 Leu Gln Pro Tyr Arg Gln Ala Leu Leu Asp Leu Glu Gln Glu Phe Leu  
238 100 105 110  
241 Gly Asp Pro His Leu Ser Ile Ser His Val Asn Tyr Phe Leu Asp Gln  
242 115 120 125  
245 Phe Gln Leu Leu Phe Pro Ser Val Met Val Val Val Glu Gln Ile Lys  
246 130 135 140  
249 Ser Gln Lys Ile His Gly Cys Gln Ile Leu Glu Thr Val Tyr Lys His  
250 145 150 155 160  
253 Ser Cys Gly Gly Leu Pro Pro Val Arg Ser Ala Leu Glu Lys Ile Leu  
254 165 170 175  
257 Ala Val Cys His Gly Val Met Tyr Lys Gln Leu Ser Ala Trp Met Leu  
258 180 185 190  
261 His Gly Leu Leu Leu Asp Gln His Glu Glu Phe Phe Ile Lys Gln Gly  
262 195 200 205  
265 Pro Ser Ser Gly Asn Val Ser Ala Gln Pro Glu Glu Asp Glu Asp  
266 210 215 220  
269 Leu Gly Ile Gly Gly Leu Thr Gly Lys Gln Leu Arg Glu Leu Gln Asp  
270 225 230 235 240  
273 Leu Arg Leu Ile Glu Glu Glu Asn Met Leu Ala Pro Ser Leu Lys Gln  
274 245 250 255  
277 Phe Ser Leu Arg Val Glu Ile Leu Pro Ser Tyr Ile Pro Val Arg Val  
278 260 265 270  
281 Ala Glu Lys Ile Leu Phe Val Gly Glu Ser Val Gln Met Phe Glu Asn  
282 275 280 285

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285 Gln Asn Val Asn Leu Thr Arg Lys Gly Ser Ile Leu Lys Asn Gln Glu  
 286 290 295 300  
 289 Asp Thr Phe Ala Ala Glu Leu His Arg Leu Lys Gln Gln Pro Leu Phe  
 290 305 310 315 320  
 293 Ser Leu Val Asp Phe Glu Gln Val Val Asp Arg Ile Arg Ser Thr Val  
 294 325 330 335  
 297 Ala Glu His Leu Trp Lys Leu Met Val Glu Glu Ser Asp Leu Leu Gly  
 298 340 345 350  
 301 Gln Leu Lys Ile Ile Lys Asp Phe Tyr Leu Leu Gly Arg Gly Glu Leu  
 302 355 360 365  
 305 Phe Gln Ala Phe Ile Asp Thr Ala Gln His Met Leu Lys Thr Pro Pro  
 306 370 375 380  
 309 Thr Ala Val Thr Glu His Asp Val Asn Val Ala Phe Gln Gln Ser Ala  
 310 385 390 395 400  
 313 His Lys Val Leu Leu Asp Asp Asp Asn Leu Leu Pro Leu Leu His Leu  
 314 405 410 415  
 317 Thr Ile Glu Tyr His Gly Lys Glu His Lys Ala Asp Ala Thr Gln Ala  
 318 420 425 430  
 321 Arg Glu Gly Pro Ser Arg Glu Thr Ser Pro Arg Glu Ala Pro Ala Ser  
 322 435 440 445  
 325 Gly Trp Ala Ala Leu Gly Leu Ser Tyr Lys Val Gln Trp Pro Leu His  
 326 450 455 460  
 329 Ile Leu Phe Thr Pro Ala Val Leu Glu Lys Tyr Asn Val Val Phe Lys  
 330 465 470 475 480  
 333 Tyr Leu Leu Ser Val Arg Arg Val Gln Ala Glu Leu Gln His Cys Trp  
 334 485 490 495  
 337 Ala Leu Gln Met Gln Arg Lys His Leu Lys Ser Asn Gln Thr Asp Ala  
 338 500 505 510  
 341 Ile Lys Trp Arg Leu Arg Asn His Met Ala Phe Leu Val Asp Asn Leu  
 342 515 520 525  
 345 Gln Tyr Tyr Leu Gln Val Asp Val Leu Glu Ser Gln Phe Ser Gln Leu  
 346 530 535 540  
 349 Leu His Gln Ile Asn Ser Thr Arg Asp Phe Glu Ser Ile Arg Leu Ala  
 350 545 550 555 560  
 353 His Asp His Phe Leu Ser Asn Leu Leu Ala Gln Ser Phe Ile Leu Leu  
 354 565 570 575  
 357 Lys Pro Val Phe His Cys Leu Asn Glu Ile Leu Asp Leu Cys His Ser  
 358 580 585 590  
 361 Phe Cys Ser Leu Val Ser Gln Asn Leu Gly Pro Leu Asp Glu Arg Gly  
 362 595 600 605  
 365 Ala Ala Gln Leu Ser Ile Leu Val Lys Gly Phe Ser Arg Gln Ser Ser  
 366 610 615 620  
 369 Leu Leu Phe Lys Ile Leu Ser Ser Val Arg Asn His Gln Ile Asn Ser  
 370 625 630 635 640  
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 374 645 650 655  
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**VERIFICATION SUMMARY**

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